



Docket No.: UTSD:1276USC1
 Serial No.: 09/686,346
 Inventor(s): Cobb et al.
 Title: "TAO Protein Kinase Polypeptides and Methods of Use Therefor"

1 TCTCGAGTATGGTAGATTATTATTCGATTATGCCAGTGGCTCATTCATACAGATGAACCAAGCTTGGATAGCAGTATAAAATTAGAATCAGACAGCTGACTGCTC
 115 AGCAGGATGCCATCACTAACAGAGCAGGCAGTCAAAGGACCCCTGAAATCGCAGAGCTCTCTCAAGAAGATCCGGAAAACCTCTCACAGATCTCAGAGAAATCGGCAAT
 MP S T N R A G S L K D P E I A E L F F K E D P E K L F T D L R E I G H 36

229 GGGGCTTGGAGCAGTTATTTGACAGAGATGCGCTACTAATGAAGTGGTGGCCATCAAGAAAATGCTTATAGTGGAAAGCAGTCTACTGAGAAATGGCAGGATATTATT
 GS F G A V Y F A R D V R T N E V V A E K K M S Y S G K Q S T E K W O D I I 74

343 AAGGAAGTCAGTTTACAAAATAAAACATCCAAAGTATAAAATCAAAGGCTCTTACGTGAACACACAGCATGCTGTTGAATGGAATATGTTAGGATCTGCT
 KE V K F L Q R I K H P N S I E Y K G C Y L R E H T A W L V M E Y C L G S A 112

457 TCGGATTACTAGAGTCATAAAAAGCATTACAAAGTGGAAATGCAGCAATTACACATGCTGCTCCAGGGATTAGCTTATTCATACCATGATCATAGA
 S D L L E V H K K P L Q E V E I A A I T H G A L O G L A Y L H S H T M I H R 150

571 GATATCAAAGCAGGAATATCCTCTGACAGAACCGCCAAGTGAACCTGGCTGACTTGGATCTGCTCCATGGCTCCCTGCCAATTCTTGAGGAAACCCATATTGG
 D I K A G N I L L T E P G Q V K L A D F G S A S M A S P A N S F V G T P Y W 188

685 ATGGCCCAGAAGTAATTAGCCATGGATGAAGGACAATATGAGGAAAGTGTGATGGTCTCTGGAATAACATGTTAGGAACTAGCCGAGAGGAAGCCCTTTATT
 M A P E V I L A M D E G Q Y D G K V D V W S L G I T C I E L A E R K P P L F 226

799 AATATGAATGCAATGAGTCCTTATATCACATAGCCAAAATGAATCCCCTACACTACAGTCTAATGAATGGCTGATTATTCGAAACTTGTAGATTCTGCTCCAGAAA
 NM N A M S A L Y H I A Q N E S P T L Q S N E W S D Y F R N F V D S C L Q K 264

913 9ATCCCTCAAGTCGCCCTACATCAGAGGAACCTTAAAGCACATGTTGCTCGAGAGCCCTGAAACAGCTGTTAATAGCTTATCAAGGACAAGGATGAGTAAGA
 I P Q D R P T S E E L L K H M F V L R E R P E T V L I D L I Q R T K D A V R 302

1027 GAGCTGAGAACATCTACAAATATGAAAGATGAGAAACTCTTCCAGGAGGACACATATGAGAACAGTAGAGAAGLACAGAGAGAGAGGAGGAGAACATGCTGCTG
 E L D N L Q Y R K M K K L L F Q E A H H N G P A V E A Q E E E E E O D H G G G 340

1141 CGGACAGAACAGTAAATAGTGTGGAAGCAATCAGTCTATCCCCAGTATGCTATCAGTGGCAGTAGCCAAGCAGCAGTGTAAAGTCTCCAGATGCTGGATGACAAG
 R T G T V N S V G S N Q S I P S M S I S A S S Q S S S V N S L P O A S D O K 378

1255 AGTGAGCTAGACATGAGGGAGGACCATACAGTGTGCTAACAGTCTGCTCATCCACTAAAACCTGAGGAGAAATTACCAAGAAGAAGGAGATCTAGAACAAGAGCA
 S E L D M M E G D H T V M S N S S V I H L K P E E E N Y Q E E G D P R T R A 416

1368 TCAGCTCACAGTCTCACCTCAAGTGTCTGTCACAAATCACATTCTGTAATAGAGAACACTTGCACACTACGAAACAGCATCTGGTAAAGAGAGCTAAGAGAACAT
 S A P Q S P P Q V S R H K S H Y R N R E H F A T I R T A S L V T R Q M Q E H 454

1483 GAGCAGGACTCTGAACTTAGAGAACAGATGTCGTTATAAGCGGATGAGGCGACAGCATCAGAGCAGCTGAGGAGAAACTGAGGAGAAATGGAGAACAT
 E Q D S E L R E Q M S G Y K R M R R Q H Q K Q L M T L E N K L K A E M D E H 492

1597 CGGCTAGATTAGACAAAGATCTGAAACACTAGCGCAACATTCTGCTGAGAAACTTAAAGAAACACCAAGCTCTATGGAAAAAGAGGCTAAAGTGTG
 R L R L D K D L E T Q R N N F A A E M E K L I K K H Q A S M E K E A K V M A 530

FIG. 1



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1711 AACGAGGAGAAAAATTCCAAACACACATTCAAGCTAACAGAAGAAAAGACTGAATAGTTTGGAGTCAAAAAGAGAATAAACTTGAAAGAGCAGCTTAAGGAG
 N E E K K F Q Q H I Q A Q Q K K E L N S F L E S Q K R E Y K L R K E Q L K E 568

1825 GAGCTGAATGAAAACCAGAGCACCTAAAAAGAAAAGCAGGAATGGCTTCAAAGCAGAAGGAGAATTCAACATTTCAGGCAGAAGAAGAGCTAATCTCTTGACGT
 E L N E N O S T P K K E K Q E W L S K O K E N I O H F O A E E E A N L L R R 606

1939 CAAAGGCGAGTCTAGAGCTAGAATGCTGCGTCAAAAGAAGAATGTTACTTGCTGGCATACTGGAACAGGACCTTGTCAGGGAGGAGTTAACAAAAGGCGAGCTCG
 Q R O Y L E L E C R R F K R R M L L G R H N L E Q D L V R E E L N K R Q T O 644

2053 AAGGACTTAAACATGCAATGTTACTGGCACAGCATGAATCCATGCAAGAACGGATTGGAGTTTCGCCACCTCAACACTATTCAAAGATGGCTGTAGTTGTCAGACTGCAACAT
 K O L E H A M L L R Q H E S M Q E L E F R H L N T I Q K M R C E L I R L O H 682

2167 CAAACTGACTACTAACCGAGCTGAATAACAATAAGAGAACGGAAACGGAAACTAACGGAAACATGTCATGGAAGTTGCACAGCAGCCTAACAGAGTTGAGCTAAAGAACCTC
 Q T E L T N Q L E Y N K R R E R E L R R K H V M E V R Q Q P K S L K S K E L 720

2281 CAAATAAAAAGCAGTTTCAGATAACCTGCAAAATTCAAACAGAGCTAACAGCTAACAGCTAACACCAAAAGACTAACACCAAAAGAGTGAGCACAAAGCTGTTCTGAAA
 Q I K K Q F Q D T C K I Q T R Q Y K A L R N H L E T T P K S E H K A V L K 758

2395 AGACTCAAGGAGGAACAGACTCGGAAGTTAGCCATTTGGCTGAGCAGTATGATCATAGCTTAATGAAATGCTCTCCACACAAGCTCTGGTTGGATGAAGCACAGGAAGCA
 R L K E E Q T R K L A I L A E Q Y D H S I N E M L S T Q A L R L D E A O E A 796

2509 GAATGCCAGGTTTGAGATGAGCTACAGGAGAACGGACTGGAGCTTGATGATCATAGGCAAAATCAAGATGAGCTGAGGCCAACATGATCGAGCTTGAGAGCTG
 E C Q V L K M Q L Q Q E L E L L N A Y Q S K I K M Q A E A Q H D R E L R E L 834

2623 GAACAAAGGTCTCCCTCGGAGAGCACTTAAACAGAAGATTGAGAAGAGATGTTGGCTTGCAGAATGACGACAGAACGAAATCGTAGCCTGCTGAGGCCAGGCC
 E Q R V S L R R A L L E Q K I E E E M L A L Q N E R T E R I R S L L E R O A 872

2737 AGAGAAATTGAGCTTGTACTGAAAGCATGAGATTAGTTAGTAACATGGCTTCTAATCTCTCCCTGAGGATTAGCCACAGCTCCAGGAGCTTCTAGCTGG
 R E I E A F D S E S M R L G F S N M V L S N L S P E A F S H S Y P G A S S W 910

2851 TCTCACATCTACTGGGGTTCAGGACCTACTGGGTCACTCCATGGGTGGCACACCCACAAGCTGGGGCATCCGATGCAAGGGAGGCCAACATGGGTACCCCTCA
 S H N P T G G S G P H W G H P M G G T P Q A W G H P M Q G G P Q P W G H P S 948

2965 GGCCAAATGCAAGGGTACCTCGAGGTAGCATAGGAGTCGGCAATAGCCCCAGGCTGAGGCGGACAGCTCTGGGGAGGGAGGGACAGGGCATGAGGAGCAG
 G P M Q G V P R G S S I G V R N S P Q A L R R T A S G G R T E Q G M S R S T 986

3079 AGTGTCACTCACAAATCCATGGTCACATGTCATACATAATAATTGAAAGTGGCAATTCCGCTGGAGCTGTCGCCAAAGAAAAGACTGCCTACAGACATCAGCACAGC
 S V T S Q I S N G S H M S Y T * * 1001

3193 CAGCCTCTCACTGGGTACTACGGGTGGAGCTGTCATATGGTATATTTCGTCCTTGTAAAGCGTTATGTTGTGTTACTAATGGATGTCAGTATTTGGCTG

FIG.1 Cont.



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	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
TA01	MPSTNRAGSIKOPETIAELFFKEDPEPKLFTIDIREIGHGSFCAVYFARDVRTNEWAIIKKMSSGKQSTEMK--QDIKEV 77										
TA02.	MPAGGRAGSIKOPDVAEELFFKDDPEPKLFSIUREIGHGSFCAVYFARDVNSEWAIIKKMSSGKQSNERK--QDIKEV 77										
ceTOA	-MAPAVILOKPGVIRDPSIHALFSNKDPEQDIREIGHGSFCAVYFAYDKNREQTVAIIKKMSSGKQAVERK--NDIKEV 76										
STE20	REERERRKKQQLYAKLINEICSDGPSTKRYANLVKIGQASGGVTAIEIGINVSAIKOMNL-EOPKKELLINEFLVMK 670										
TA01	KELQRRIKHPNSIEYKGCYLREHTANLVMWCLGASDILLEVHKKPLQEVEVIAITHGALQGLAYLHSHTMHLRDIKAGN 156										
TA02	REFOKLRHPNTIQVRGCGYLREHTANLVMWCLGASEEFLVHKKPPLQEVEVIAAVTHGALQGLAYLHSHTMHLRDIKAGN 156										
ceTOA	SEINTVVPHPHIVDYKACFLMDTTCTCLVMEWICGSAADIVLVRKGHREVEVIAICSQTLDALRYLHSLSKRHLRDIKAGN 155										
STE20	G---SKHRPNTVNFDTSVYLKGDWVIMEWEGESTDV-VTHCLITEQIGAVCRETSASIEFHHSKGVLHRDIKSDN 744										
TA01	ILLTEPGVYKLADFGSAS---MASPANSVTGTPYWWAPEVILAMDEGQYDGKVVDWSLIGITCIELAERKPLFMNA 230										
TA02	ILLSERPGVYKLADFGSAS---IMAPANSVTGTPYWWAPEVILAMDEGQYDGKVVDWSLIGITCIELAERKPLFMNA 230										
ceTOA	ILLSDHAIYVYLADFGSAS---LVDPAQFTIGTPYWWAPEVILAMDEGHTDRADIWSLIGITCIELAERRPLFSMNA 229										
STE20	ILLSMSEGDIKLTDGFCAQINELNKRTTMVGTPYWWAPEVSRKE---YGPKVDTWSLGMIMIEMIESPPVYNETP 819										
TA01	MSALYHIAQMESPTLQSNEWSDIFRN-----FUDSCLOKIPQDRPTSE 273										
TA02	MSALYHIAQNEPALSQSGHSEYFRN-----FUDSCLOKIPQDRPTSE 273										
ceTOA	MSALYHIAQNDPPTLSPIDYSEQPWSLEVFOIDKCLRPAEEFMSAE 279										
STE20	IRALYLIATNGTPKLUKEPNLSS---SLRK--FUDWCICLVEPEDRASAT 863										

FIG. 2



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Title: "TAO Protein Kinase Polypeptides and Methods of Use Therefor"

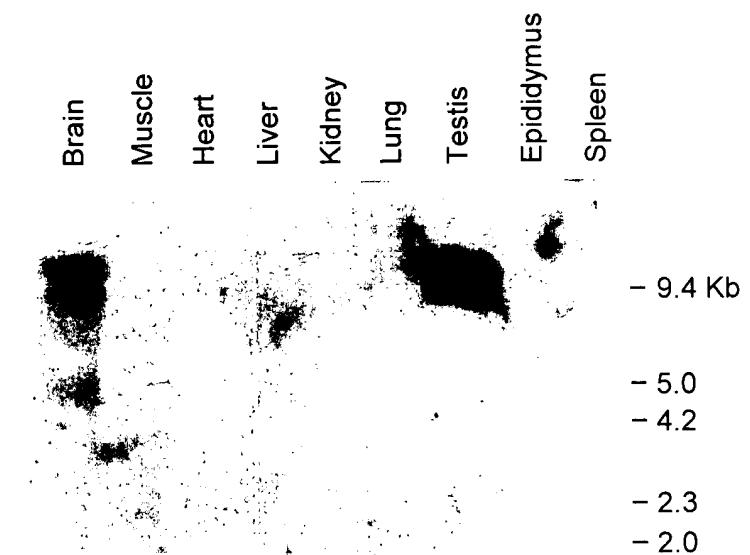


FIG.3A

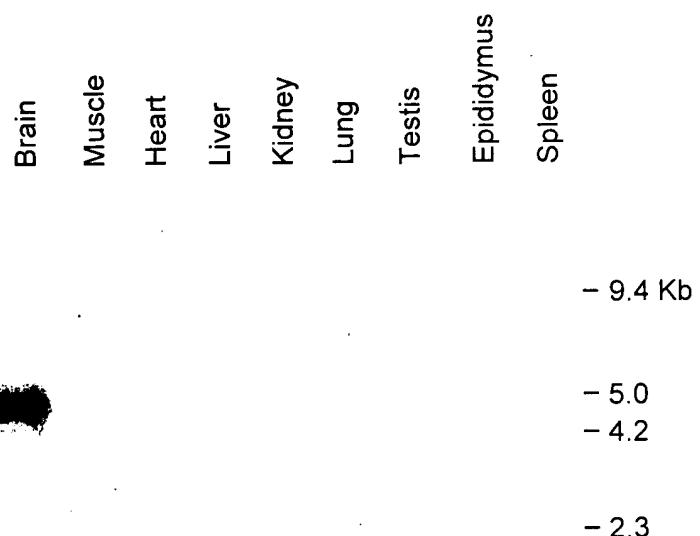


FIG.3B

FIG. 4A

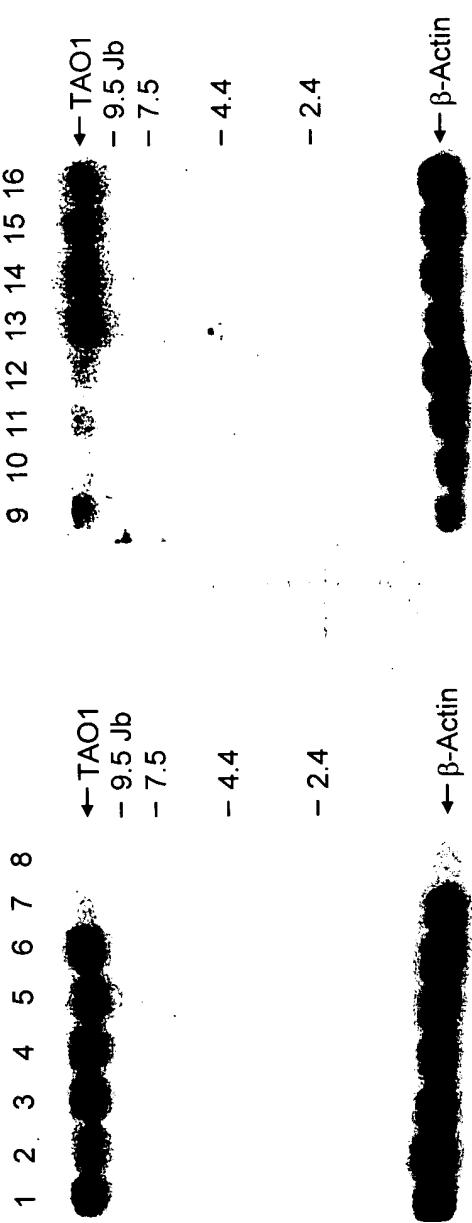


FIG. 4B



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Title: "TAO Protein Kinase Polypeptides and Methods of Use Therefor"



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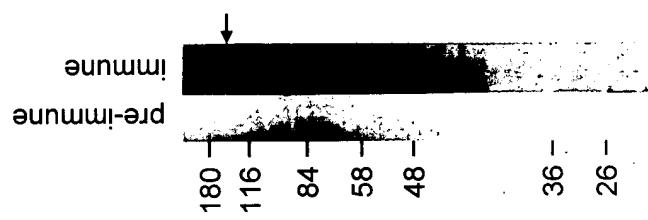
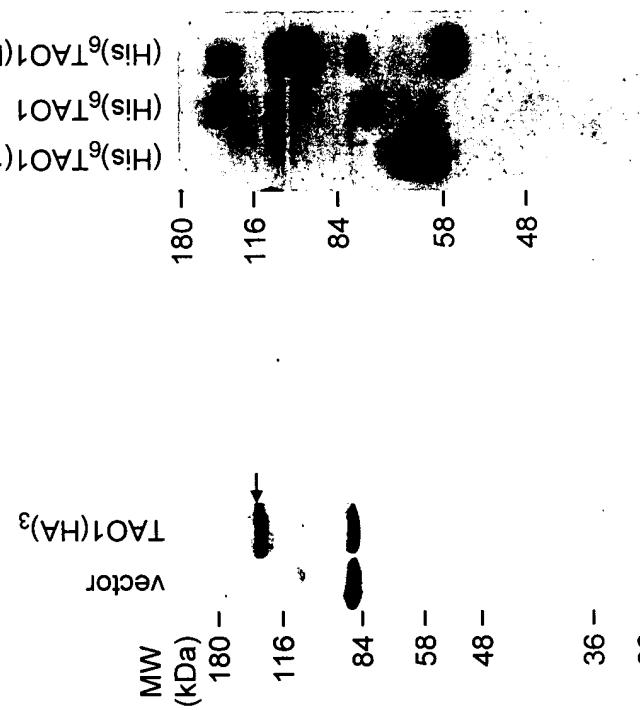


FIG. 5C

FIG. 5B

FIG. 5A





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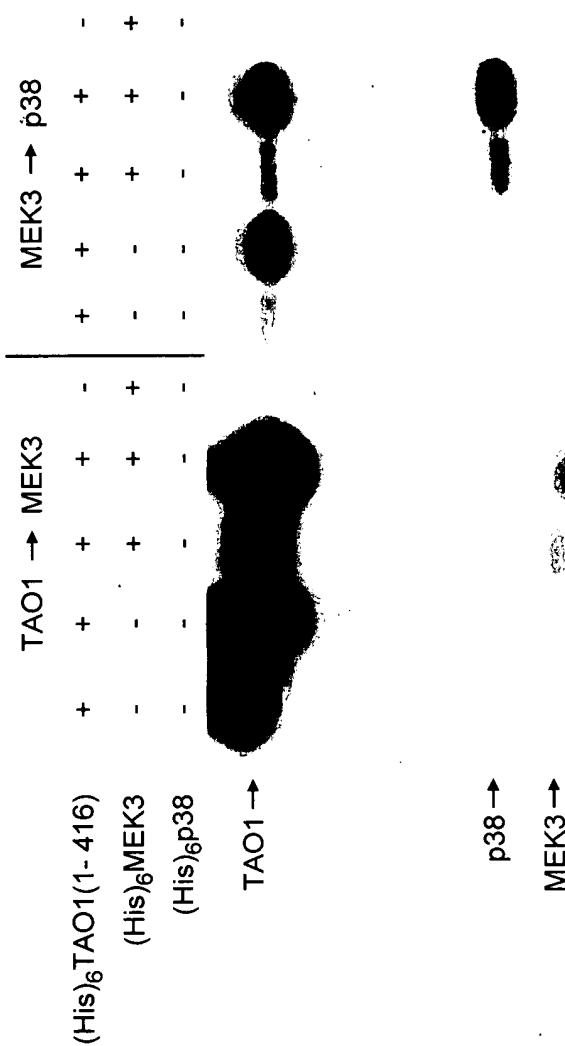


FIG. 6

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Inventor(s): Cobb et al.

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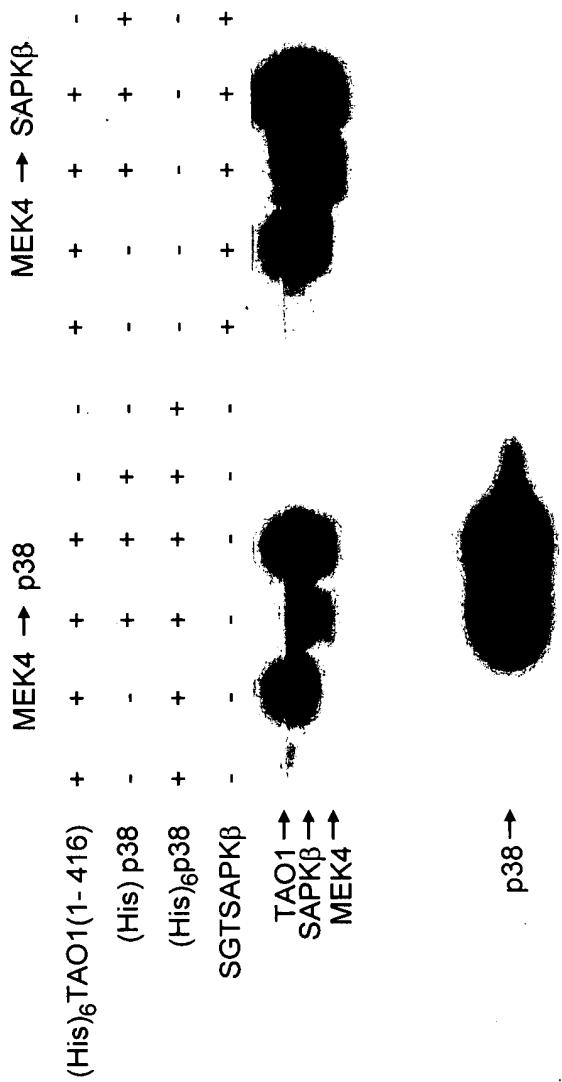


FIG. 7



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	MEK6 → p38			
(His) ₆ TAQ1(1-416)	+	+	-	-
GSTMek6	-	+	+	-
(His) ₆ p38	+	+	+	+

TAO1 → [REDACTED]

MEK6 →

p38 → [REDACTED]

FIG.8



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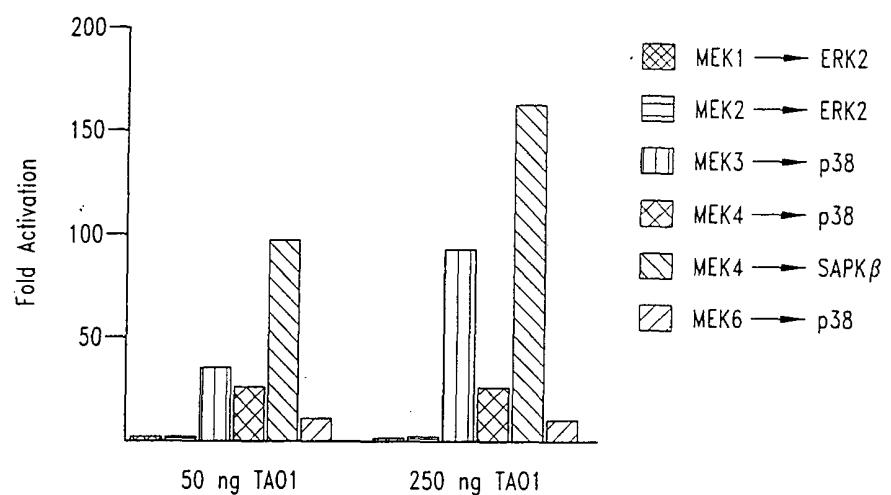


FIG.9



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vector	+	+	-	-
pCMV5TAO1(HA) ₃	-	-	+	+
pCMV5mycMEK3	-	+	+	+



FIG.10

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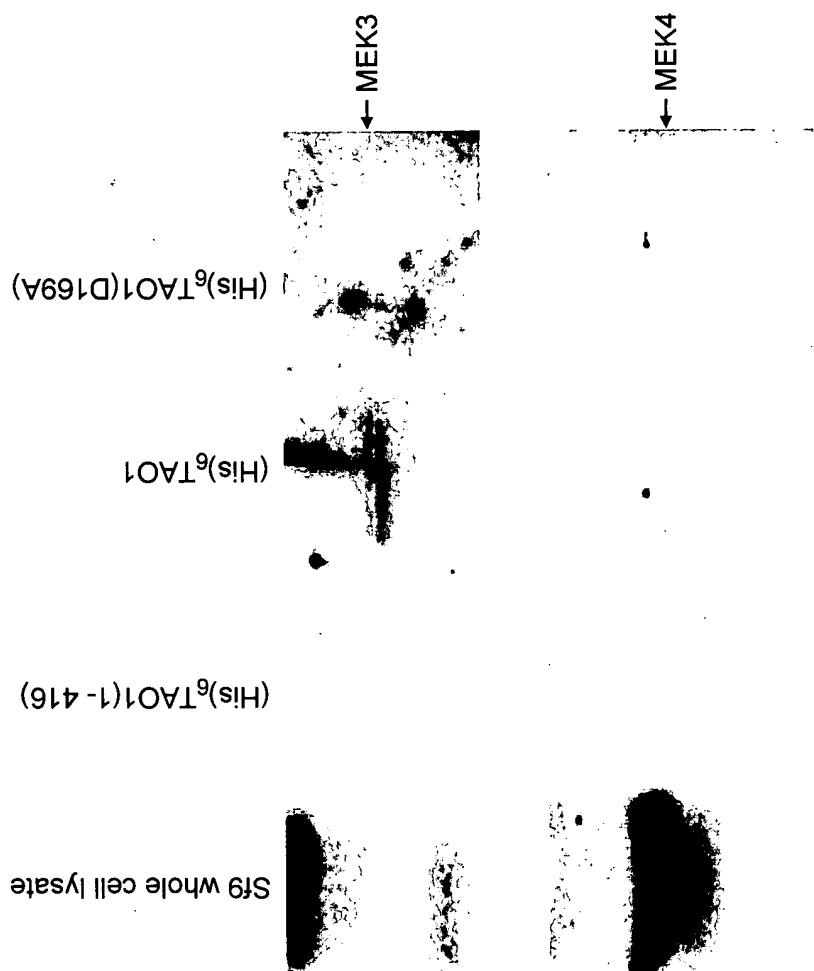


FIG. 11



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Query: 2341 AGGAATCACCTACTGGAGACTACACCAAAGAGTGAGCACAAAGCTGTTCTGAAAAGACTC 2400
Sbjct: 12 ACGANTCACCAGTTGGAAGTTACTCCAAAGAATGAGCACAAAACAATCTAAAGACACTG 71

Query: 2401 AAGGAGGAACAGACTCGGAAGTGTAGGCCATCTGGCTGAGCAGTATGATCATAGCATTAAAT 2460
Sbjct: 72 AAAGATGAGCAGACAAGAAAATGCCATTNGGCAGAGCAGTATGAACAGAGTATAAT 131

Query: 2461 GAAATGCTCTCACACAAGCTCTCGCTTGGATGAAGCACAGGAAGCAGAATGCCAGTT 2520
Sbjct: 132 GAAATGATGGCTCTCANGCGTTACGGCTAGATGAGGCTCAAGAACGAGAATGCCAGGCC 191

Query: 2521 TTGAAGATGAGCTACAGCAGGAACCTGGAGCTGTTGAATGCATATCAGAGCAAATCAAG 2580
Sbjct: 192 TTGAGGCTACAGCTCAGCAGGAAATGGAGCTGCTCAACGCCCTACAGAGCAAATCAAG 251

Query: 2581 ATGCAGGCTGAGGCCAACATGATCGAGAGCTTCGAGAGCTGGAACAAAGGGTCTCCCTT 2640
Sbjct: 252 ATGCAACACAGAGGCAACATGAACGTGAGCTCCAGAAGCTAGAGCAGAGAGTGTCTCTG 311

Query: 2641 CGGAGAGCACTTTAGAACAGAACAGATTGAAGAACAGAGATGTTGGCTTGCAGAACG 2700
Sbjct: 312 CGCACAGCACACCTTGAGCCAGAACATTGAAGAGGAGCTGGCTGCCCTCAGAACG 371

Query: 2701 ACAGAACGAATACGTAGCCTGCTCGAGGCCAGGCCAGAGAAATTGAAGCTTT 2754
Sbjct: 372 AGCGAGAGAATAAGAACCTATTGAAAGGCAAGAGCAGAGATTGAAACTTT 425

FIG. 12



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Query: 964 GAACAAACATGTGCTTAAAGTTCTCTGATGTAGGGCATCTTGAGGGATTTCTGGA 905
||||||| ||||| ||||| |||||
Sbjct: 79 GAACAAAGTCATGCCTTAATAAGTTCTGCTGATGTTGGCTTCCTGAGGTATTTCTGCA 138

Query: 904 GGCAAGAATCTACAAAGTTGAAAATAATCAGACCATTCTAGACTGTAGTAGTGGG 845
||| ||||| ||||| |||||
Sbjct: 139 AGCAGTAATCAACAAATCTCTAAAGGAGCTGTCCATTCTAGACTGTAAACGTTGGG 198

Query: 844 ATTCACTTGGCTATGTGATATAAGGCACTATTGCAATTATTAATAAGGAGGCT 785
||||||| ||||| ||||| |||||
Sbjct: 199 AGTCATTCTGGCAATGTGATATAAGGCACTATTGCAATTGTTGAAAAGGGCGGCT 258

Query: 784 TCCCTCGGCTAATTCAACATGTTTCCAAAGAGACCATACATCAACTTGCATCAT 725
||| ||||| ||||| |||||
Sbjct: 259 TCCGTTCCGCCAATTCAACAAAGTGTGCAAGTGACCAAATATCAACTTCCCATCAT 318

Query: 724 ATTGTCCTTCATCCATGGCTAAATTACTTCTGGGGCATCCAATATGGTGTCCACAA 665
||||||| ||||| |||||
Sbjct: 319 ACTGTCTTCATCCATAGCTAACAGTCAGTCAAGTCAGCTGGAGCCATCCAGTAAGGTGTGCCACGA 378

Query: 664 AAGAATTGGCAGGG 651
| | | | | | | |
Sbjct: 379 AGGAGTTGCCAGG 392

FIG. 13



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Query: 2792 ACCATGTTACTAAACCTAATCTCATGCTTCAGAGTCAAAGCTCAATTCTCTGGCC 2733
|||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 90 ACCAAATTCCAAATCCATTCTGAGGCTCTCCATGTCAAAGTTCAATCTCTCGCTCT 149

Query: 2732 TGGCCTCGAGCAGGCTACGTATTCTGTTCTGCGTTCATCTGCAAAGCCAACATCTCT 2673
|||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 150 TGCCTTCAATAGGTTCTTATTCCTCGCTGCGTTCTGAAGGGCAGCCAGCTCC 209

Query: 2672 TCTTCAATCTCTGTTCTAAGAGTGCTCTCGAAGGGAGACCTTTGTTCCAGCTCTGA 2613
|||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 210 TCTTCAATCTCTGCTCAAGGTGTTCTGCGAGAGACACTCTGCTCTAGTTCTGG 269

Query: 2612 AGCTCTGATCATGTTGGGCCCTAGCCTQCATCTGATTTGCTGATATGCATTCAAC 2553
|||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 270 AGCTCACGTTCATGTTGCTGCTGTTNGNATCTGATTTGGNTCTGGTAGGGTTGAGC 329

Query: 2552 AGCTCCAGTTCTGCTGAGCTGCATCTCAAAACCTGGCATTCTGCTTCTGTGCTTC 2493
|||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 330 AGCTCCATTCTGCTGGAGCTGAGCCTCAAGGCCCTGGCATTCTGCTCTGAGCCTCA 389

Query: 2492 TCCAAACGCAGAGCTTGTGGAGAGCATTTCAATTATGCTATGATCATACTGCTCAGCC 2433
|||||| ||||| ||||| ||||| |||||
Sbjct: 390 TCTAGCCGTAACGCTTGAGAGGCCATTTCAATTATGCTCATCTGCTCTGCC 449

Query: 2432 AAGATGGCTA 2423
|||||| |
Sbjct: 450 AAAATGGCAA 459

FIG. 14



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FIG. 15A

Query: 2437 GAGCAGTATGATCATAGCTTAATGAAATGCTCTCACACAAGCTCTGCCTTGATGAA 2496
||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 193 GAGCAGTATGAACAGAGTATAATGAAATGATGGCTCTCAAGCGTTACGGCTAGATGAG 252

Query: 2497 GCACA 2501
|| |
Sbjct: 253 GCTCA 257

FIG. 15B



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Query:	2087	ATGAATCCATGCAAGAACTGGAGTTGCCACCTCAACACTATTCAAGAGATGCGCTGTG	2146
Sbjct:	31	ACGAGTCCCCGGAGAGCTAGAGTACAGGCAGCTGCACACGTTACAGAAGCTACGCATGG	90
Query:	2147	AGTTGATCAGACTGCAACATCAAACGTAGCTTAACCACTGGAAATACAATAAGAGAA	2206
Sbjct:	91	ATCTGATCCGTTACAGCACCAAGCGAACCTGGAAAACCAGCTGGAGTACAATAAGAGGC	150
Query:	2207	GGGAAACGGGAACTAAGACGGAAACATGTCATGGAAAGTTGCAGCAGCCTAACAGAGTTGA	2266
.			
Sbjct:	151	GAGAAAAGAGAACTGCACAGAACATGTCATGGAACTTCCGGCAACAGCaaaaAACTAA	210
Query:	2267	AGTCTAAAGAACTCCAATAAAAAGCAGTTCAGGATA	2305
Sbjct:	211	AGGCCATGGAANTGCAATTAAAAAACAGTTCCAGGAAA	249

FIG. 16



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Query: 3228 GTGCATATGGTATATTTATTCTCTTTGTAAGCGTTATGTTTGTTACTAATTGG 3287

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 31 GTGCATATGGTATATTTNATTCACTTTGTAAGCGTTCTGTTTGTTACTAATTGG 90

Query: 3288 GATGTCATACTATTTGGCTGCCGGG 3312

||||||| ||||| ||||| |||||

Sbjct: 91 GATGTCATACTACTTGGCTGCCGGG 115

FIG.17A

Query: 3200 CTCACTTGGGTACTACCCGGGTGGAAGCTGTGCATATGGTATATTT 3245

||||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 1 CTCACTTGGGTACTACAGTGGAAGCTGAGTGCAATGGTATATT 46

FIG.17B



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FIG. 18



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FIG. 19A

FIG. 19B



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FIG.20